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Sequence Listing was accepted.

See attached Validation Report.

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Reviewer: Anne Corrigan

Timestamp: [year=2008; month=3; day=26; hr=20; min=1; sec=13; ms=756; ]

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Application No: 10556669 Version No: 1.1

Input Set:

Output Set:

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Finished: 2008-03-26 19:59:33.394  
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Total Warnings: 4  
Total Errors: 0  
No. of SeqIDs Defined: 10  
Actual SeqID Count: 10

Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (10)

# SEQUENCE LISTING

<110> PURDUE RESEARCH FOUNDATION  
Bressan, Roy A

<120> METHODS AND COMPOSITIONS TO INCREASE PLANT  
RESISTANCE TO STRESS

<130> 12558-0072

<140> 10556669

<141> 2008-03-14

<150> PCT/US04/10599

<151> 2004-04-07

<150> 60/461,345

<151> 2003-04-09

<160> 10

<170> PatentIn version 3.5

<210> 1

<211> 211

<212> PRT

<213> Arabidopsis thaliana

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Trp Thr Lys Glu Glu Asp Gln Arg Leu Ile Asp Tyr Ile Arg Asn His  
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Gly Glu Gly Ser Trp Arg Ser Leu Pro Lys Ser Val Gly Leu Leu Arg  
35 40 45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp  
50 55 60

Leu Lys Arg Gly Asn Phe Thr Asp Gly Glu Glu Gln Ile Ile Val Lys  
65 70 75 80

Leu His Ser Leu Phe Gly Asn Lys Trp Ser Leu Ile Ala Gly Lys Leu  
85 90 95

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Ile  
100 105 110

Lys Arg Lys Leu Leu Asn Arg Gly Ile Asp Pro Lys Thr His Gly Ser  
 115 120 125

Ile Ile Glu Pro Lys Thr Thr Ser Phe His Pro Arg Asn Glu Asp Leu  
 130 135 140

Lys Ser Thr Phe Pro Gly Ser Val Lys Leu Lys Met Glu Thr Ser Cys  
 145 150 155 160

Asn Cys Ala Ser Thr Ser Gly Thr Thr Thr Asp Glu Asp Leu Arg Leu  
 165 170 175

Ser Val Asp Cys Asp Tyr Arg Tyr Asp His Leu Asp Lys Glu Leu Asn  
 180 185 190

Leu Asp Leu Thr Leu Gly Tyr Ser Pro Thr Arg Phe Val Gly Val Gly  
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Ser Cys Tyr  
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 cctaaatccg ttgggttggt gcgttggtga aaaagttgta gattaagatg gattaattac 180  
 cttcgtcctg atcttaaacg tggaaatttc actgatggtg aagagcaaatt cattgtcaaa 240  
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 gataatgaga ttaaaaatta ttggaacact catataaaaa ggaagcttct taaccgtggt 360  
 attgacccaa aaactcacgg ttcgatcatc gagcctaaaa cgacatcggt tcatccccga 420  
 aatgaagatt tgaagtccac gtttcccggt tctgttaaac taaagatgga gacttcttgt 480  
 gaaaactgtg cttctacgag cggtagcact acggacgagg atttacggtt aagtgttgat 540  
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Trp Thr Lys Glu Glu Asp Gln Arg Leu Val Asp Tyr Ile Arg Asn His  
20 25 30

Gly Glu Gly Cys Trp Arg Ser Leu Pro Lys Ser Ala Gly Leu Leu Arg  
35 40 45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp  
50 55 60

Leu Lys Arg Gly Asn Phe Thr Asp Asp Glu Asp Gln Ile Ile Ile Lys  
65 70 75 80

Leu His Ser Leu Leu Gly Asn Lys Trp Ser Leu Ile Ala Gly Arg Leu  
85 90 95

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Ile  
100 105 110

Lys Arg Lys Leu Leu Ser His Gly Ile Asp Pro Gln Thr His Arg Gln  
115 120 125

Ile Asn Glu Ser Lys Thr Val Ser Ser Gln Val Val Val Pro Ile Gln  
130 135 140

Asn Asp Ala Val Glu Tyr Ser Phe Ser Asn Leu Ala Val Lys Pro Lys  
145 150 155 160

Thr Glu Asn Ser Ser Asp Asn Gly Ala Ser Thr Ser Gly Thr Thr Thr  
165 170 175

Asp Glu Asp Leu Arg Gln Asn Gly Glu Cys Tyr Tyr Ser Asp Asn Ser  
180 185 190

Gly His Ile Lys Leu Asn Leu Asp Leu Thr Leu Gly Phe Gly Ser Trp

195

200

205

Ser Gly Arg Ile Val Gly Val Gly Ser Ser Ala Asp Ser Lys Pro Trp  
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Cys Asp Pro Val Met Glu Ala Arg Leu Ser Leu Leu  
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&lt;212&gt; PRT

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Trp Thr Lys Glu Glu Asp Gln Arg Leu Ile Asn Tyr Ile Arg Val His  
 20 25 30

Gly Glu Gly Cys Trp Arg Ser Leu Pro Lys Ala Ala Gly Leu Leu Arg  
 35 40 45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp  
 50 55 60

Leu Lys Arg Gly Asn Phe Thr Glu Glu Glu Asp Glu Leu Ile Ile Lys  
 65 70 75 80

Leu His Ser Leu Leu Gly Asn Lys Trp Ser Leu Ile Ala Gly Arg Leu  
 85 90 95

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Ile  
 100 105 110

Lys Arg Lys Leu Ile Ser Arg Gly Ile Asp Pro Gln Thr His Arg Pro  
 115 120 125

Leu Asn Gln Thr Ala Asn Thr Asn Thr Val Thr Ala Pro Thr Glu Leu  
 130 135 140

Asp Phe Arg Asn Thr Pro Thr Ser Val Ser Lys Ser Ser Ser Ile Lys  
 145 150 155 160

Asn Pro Ser Leu Asp Phe Asn Tyr Asn Glu Phe Gln Phe Lys Ser Asn  
165 170 175

Thr Asp Ser Leu Glu Glu Pro Asn Cys Thr Thr Ser Ser Gly Met Thr  
180 185 190

Thr Asp Glu Glu Gln Gln Glu Gln Leu His Lys Gln Gln Gln Tyr Asp  
195 200 205

Pro Ser Asn Gly Gln Asp Leu Asn Leu Glu Leu Ser Ile Gly Ile Val  
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Ser Ala Asp Ser Ser Arg Val Ser Ser Ala Asn Ser Ala Glu Ser Lys  
225 230 235 240

Pro Lys Val Asp Asn Asn Asn Phe Gln Phe Leu Glu Gln Ala Met Val  
245 250 255

Ala Lys Ala Val Cys Leu Cys Trp Gln Leu Gly Phe Gly Thr Ser Glu  
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Ile Cys Arg Asn Cys Gln Asn Ser Asn Ser Asn Gly Phe Tyr Ser Tyr  
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Cys Arg Pro Leu Asp Ser  
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Trp Thr Lys Glu Glu Asp Gln Arg Leu Ile Ala Tyr Ile Arg Ala His  
20 25 30

Gly Glu Gly Cys Trp Arg Ser Leu Pro Lys Ala Ala Gly Leu Leu Arg  
35 40 45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Met Asn Tyr Leu Arg Pro Asp

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Leu Lys Arg Gly Asn Phe Thr Asp Asp Glu Asp Glu Leu Ile Ile Arg  
 65 70 75 80

Leu His Ser Leu Leu Gly Asn Lys Trp Ser Leu Ile Ala Gly Gln Leu  
 85 90 95

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Ile  
 100 105 110

Lys Arg Lys Leu Leu Ala Arg Gly Ile Asp Pro Gln Thr His Arg Pro  
 115 120 125

Leu Leu Ser Gly Gly Asp Gly Ile Ala Ala Ser Asn Lys Arg His His  
 130 135 140

Arg Arg Arg Ile Pro Tyr Pro Ser Arg Arg Arg Arg Arg Pro Arg Arg  
 145 150 155 160

Ser Ser Pro Cys Glu Ala Ala Ala Ala Ala Ala Pro Gly Arg Leu Leu  
 165 170 175

Gly Arg Arg Leu Pro Gln Gln Gln Arg His Asn Glu His Gly Gly Ala  
 180 185 190

Ala Val Pro Arg Pro Gln Pro Arg Ala Leu Gly Arg Ala Asp Ala Glu  
 195 200 205

Leu Ala Ala Gly Gly Asp Ala His Gln Arg Ala Ala Gly Leu Pro Leu  
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Leu Pro Pro Arg Leu Pro Arg Arg Gly Gly Val Gln Leu Ser Gly  
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<211> 273

<212> PRT

<213> Lycopersicon esculentum

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Trp Thr Lys Glu Glu Asp Glu Arg Leu Ile Ser Tyr Ile Arg Ala His  
 20 25 30

Gly Glu Gly Cys Trp Arg Ser Leu Pro Lys Ala Ala Gly Leu Leu Arg  
 35 40 45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp  
 50 55 60

Leu Lys Arg Gly Asn Phe Thr Glu Glu Glu Asp Glu Leu Ile Ile Lys  
 65 70 75 80

Leu His Ser Leu Leu Gly Asn Lys Trp Ser Leu Ile Ala Gly Arg Leu  
 85 90 95

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Ile  
 100 105 110

Arg Arg Lys Leu Leu Ser Arg Gly Ile Asp Pro Thr Thr His Arg Ser  
 115 120 125

Ile Asn Asp Pro Thr Thr Ile Pro Lys Val Thr Thr Ile Thr Phe Ala  
 130 135 140

Ala Ala His Glu Asn Ile Lys Asp Ile Asp Gln Gln Asp Glu Met Ile  
 145 150 155 160

Asn Ile Lys Ala Glu Phe Val Glu Thr Ser Lys Glu Ser Asp Asn Asn  
 165 170 175

Glu Ile Ile Gln Glu Lys Ser Ser Ser Cys Leu Pro Asp Leu Asn Leu  
 180 185 190

Glu Leu Arg Ile Ser Pro Pro His His Gln Gln Leu Asp His His Arg  
 195 200 205

His His Gln Arg Ser Ser Ser Leu Cys Phe Thr Cys Ser Leu Gly Ile  
 210 215 220

Gln Asn Ser Lys Asp Cys Ser Cys Gly Ser Glu Ser Asn Gly Asn Gly  
 225 230 235 240

Trp Ser Asn Asn Met Val Ser Met Asn Ile Met Ala Gly Tyr Asp Phe  
245 250 255

Leu Gly Leu Lys Thr Asn Gly Leu Leu Asp Tyr Arg Thr Leu Glu Thr  
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Lys

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<210> 8  
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<210> 10  
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acgttctaga cacacgagct agtaacaaga tc